



Sequence Listing

<110> Lasky, Laurence A.
Dowbenko, Donald J.

<120> Tyrosine Phosphorylated Cleavage Furrow-Associated Proteins (PSTPIPs)

<130> P1066P2

<140> US 09/068,377
<141> 1998-05-08

<150> PCT/US98/01774
<151> 1998-01-30

<150> US 08/938,830
<151> 1997-09-29

<150> US 60/104,589
<151> 1997-02-07

<160> 73

<210> 1
<211> 415
<212> PRT
<213> Mus Musculus

<400> 1

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Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu
20 25 30

Asp Gly Arg Lys Met Cys Lys Asp Val Glu Glu Leu Leu Arg Gln
35 40 45

Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
50 55 60

Ala Arg Lys Ala Gly Gly Gln Thr Glu Met Asn Ser Leu Arg Thr
65 70 75

Ser Phe Asp Ser Leu Lys Gln Gln Thr Glu Asn Val Gly Ser Ala
80 85 90

His Ile Gln Leu Ala Leu Arg Glu Glu Leu Arg Ser Leu
95 100 105

Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Tyr Glu
110 115 120

Ala Ile Met Asp Arg Val Gln Lys Ser Lys Leu Ser Leu Tyr Lys
125 130 135

Lys Thr Met Glu Ser Lys Lys Ala Tyr Asp Gln Lys Cys Arg Asp
 140 145 150
 Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Val Ser Ala Asn Gly
 155 160 165
 His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys Ala Lys Gln Cys
 170 175 180
 Lys Glu Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Asn Ile
 185 190 195
 Glu Gln Leu Glu Arg Ala Arg Thr Glu Trp Glu Gln Glu His Arg
 200 205 210
 Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe Asp Arg Leu Thr
 215 220 225
 Ile Leu Arg Asn Ala Leu Trp Val His Cys Asn Gln Leu Ser Met
 230 235 240
 Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr
 245 250 255
 Leu Glu Gly Cys Asp Val Glu Gly Asp Ile Asn Gly Phe Ile Gln
 260 265 270
 Ser Lys Ser Thr Gly Arg Glu Pro Pro Ala Pro Val Pro Tyr Gln
 275 280 285
 Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Ile Gly Ser Pro Ser
 290 295 300
 Ile Gln Pro Ser Cys Gly Val Ile Lys Arg Phe Ser Gly Leu Leu
 305 310 315
 His Gly Ser Pro Lys Thr Thr Pro Ser Ala Pro Ala Ala Ser Thr
 320 325 330
 Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Leu Val Tyr Ala
 335 340 345
 Ser Ile Glu Val Gln Ala Thr Gln Gly Asn Leu Asn Ser Ser Ala
 350 355 360
 Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp
 365 370 375
 Glu Leu Asp Ile Ser Ala Gly Asp Ile Leu Ala Val Ile Leu Glu
 380 385 390
 Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly
 395 400 405
 Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu
 410 415

<210> 2
<211> 2100
<212> DNA
<213> Mus Musculus

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gaacctcata acaactcaaa caaattctca agcgcttca caaccaattg 200
cctcctctaa cgttcatgat aacttcatga ataatgaaat cacggctagt 250
aaaattgatg atggtaataa ttcaaaacca ctgtcacctg gttggacgga 300
ccaaactgcg tataacgcgt ttggaatcac tacaggatg tttaataccca 350
ctacaatgga tgatgtatat aactatctat tcgatgatga agataacccca 400
ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gtccttcct 450
catttcgctg ctgattctag ccccaaacaa aacaggttga gccttttcc 500
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ggcgccggct gggagtggga gggagggcct gggctagccg cgctgggact 600
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caagaaggca tatgaccaga agtgcagggaa tgcagatgat gctgagcagg 1150
ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300

aggagcaccc gactacctgt gaggccttcc agttgcagga gtttgaccgg 1350
ctcaccatcc tccgcaatgc cctgtgggtg cactgtaacc agctctccat 1400
gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450
agggctgtga tgtgaaaggt gacatcaatg gcttcatcca gtccaagagc 1500
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tccctgggtc gtacttggag aagctctgag gaaaggctag cagtctccac 1950
atacctccgc cctgactgtg aggtcaggac tgtttcttcc catcaccgcc 2000
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<211> 48
<212> PRT
<213> Mus Musculus

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Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser
1 5 10 15

Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
20 25 30

Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
35 40 45

Tyr Leu Arg

<210> 4
<211> 50
<212> PRT
<213> Homo sapien

<400> 4

Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
1 5 10 15

Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
20 25 30

Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
35 40 45

Tyr Val Glu Lys Ile
50

<210> 5

<211> 50

<212> PRT

<213> Homo sapien

<400> 5

Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
1 5 10 15

Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
20 25 30

Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
35 40 45

Tyr Val Lys Lys Leu
50

<210> 6

<211> 50

<212> PRT

<213> Homo sapien

<400> 6

Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
20 25 30

Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Lys Leu Leu
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<210> 7

<211> 48

<212> PRT

<213> Homo sapien

<400> 7

Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
20 25 30
Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
35 40 45
Tyr Val Glu

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid epitope tag

<400> 8
Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 9
cgccggatcca ccatgatggc ccagctgcag ttc 33

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 10
gtacgcgtcg actcacttgt catcgctgc cttgttagtcg agctt 45

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
tgcccttctc tccacagg 18

<210> 12
<211> 36
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 12
ctccttgagg ttctactagt gggggctggg gtcctg 36

<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13
gcggccgcac tagtatccag tctgtgctcc atctgttac 39

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14
gcgtttggaa tcactac 17

<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15
ttatagttta gcggccgctc accggtagtc ctgggctgat g 41

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 16
gtacgcgtcg accgcactct acgactacac tgcacag 37

<210> 17
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
ctctggcgaa gaagtcc 17

<210> 18
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
gatcgaattc ccagaacctc aaggagaact gc 32

<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gatcctcgag ttacacccgt gtccactctg ctggagga 38

<210> 20
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 20
Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ala Glu Trp Thr
20

<210> 21
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 21
Gly Phe Gly Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro
1 5 10 15

Pro Ser Ala Trp

<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 22
Gly Phe Gly Asn Arg Cys Gly Lys Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ser Glu Trp Thr
20

<210> 23
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 23
Gly Gly Val Leu Arg Ser Ile Ser Val Pro Ala Pro Pro Thr Leu
1 5 10 15

Pro Met Ala Asp Thr
20

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
gtatatatgtcc tggccagccc atggggttcc cagcag 36

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
gcagggtcgac tctagattac acccgtgtcc actctg 36

<210> 26
<211> 907
<212> PRT
<213> *Saccharomyces Pombe*

<400> 26

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				20					25				30	
Ile	Asp	Glu	Phe	Tyr	Ala	Lys	Arg	Ala	Ser	Ile	Glu	Arg	Glu	Tyr
					35				40				45	
Ala	Ser	Lys	Leu	Gln	Glu	Leu	Ala	Ala	Ser	Ser	Ala	Asp	Ile	Pro
					50				55				60	
Glu	Val	Gly	Ser	Thr	Leu	Asn	Asn	Ile	Leu	Ser	Met	Arg	Thr	Glu
					65				70				75	
Thr	Gly	Ser	Met	Ala	Lys	Ala	His	Glu	Glu	Val	Ser	Gln	Gln	Ile
					80				85				90	
Asn	Thr	Glu	Leu	Arg	Asn	Lys	Ile	Arg	Glu	Tyr	Ile	Asp	Gln	Thr
					95				100				105	
Glu	Gln	Gln	Lys	Val	Val	Ala	Ala	Asn	Ala	Ile	Glu	Glu	Leu	Tyr
					110				115				120	
Gln	Lys	Lys	Thr	Ala	Leu	Glu	Ile	Asp	Leu	Ser	Glu	Lys	Lys	Asp
					125				130				135	
Ala	Tyr	Glu	Tyr	Ser	Cys	Asn	Lys	Leu	Asn	Ser	Tyr	Met	Arg	Gln
					140				145				150	
Thr	Lys	Lys	Met	Thr	Gly	Arg	Glu	Leu	Asp	Lys	Tyr	Asn	Leu	Lys
					155				160				165	
Ile	Arg	Gln	Ala	Ala	Leu	Ala	Val	Lys	Lys	Met	Asp	Ala	Glu	Tyr
					170				175				180	
Arg	Glu	Thr	Asn	Glu	Leu	Leu	Leu	Thr	Val	Thr	Arg	Glu	Trp	Ile
					185				190				195	
Asp	Arg	Trp	Thr	Glu	Val	Cys	Asp	Ala	Phe	Gln	His	Ile	Glu	Glu
					200				205				210	
Tyr	Arg	Leu	Glu	Phe	Leu	Lys	Thr	Asn	Met	Trp	Ala	Tyr	Ala	Asn
					215				220				225	
Ile	Ile	Ser	Thr	Ala	Cys	Val	Lys	Asp	Asp	Glu	Ser	Cys	Glu	Lys
					230				235				240	
Ile	Arg	Leu	Thr	Leu	Glu	Asn	Thr	Asn	Ile	Asp	Glu	Asp	Ile	Thr
					245				250				255	
Gln	Met	Ile	Gln	Asn	Glu	Gly	Thr	Gly	Thr	Thr	Ile	Pro	Pro	Leu
					260				265				270	
Pro	Glu	Phe	Asn	Asp	Tyr	Phe	Lys	Glu	Asn	Gly	Leu	Asn	Tyr	Asp

	275	280	285
Ile Asp Gln Leu Ile Ser Lys Ala Pro Ser Tyr Pro Tyr Ser Ser			
290	295	300	
Ser Arg Pro Ser Ala Ser Ala Ser Leu Ala Ser Ser Pro Thr Arg			
305	310	315	
Ser Ala Phe Arg Pro Lys Thr Ser Glu Thr Val Ser Ser Glu Val			
320	325	330	
Val Ser Ser Pro Pro Thr Ser Pro Leu His Ser Pro Val Lys Pro			
335	340	345	
Val Ser Asn Glu Gln Val Glu Gln Val Thr Glu Val Glu Leu Ser			
350	355	360	
Ile Pro Val Pro Ser Ile Gln Glu Ala Glu Ser Gln Lys Pro Val			
365	370	375	
Leu Thr Gly Ser Ser Met Arg Arg Pro Ser Val Thr Ser Pro Thr			
380	385	390	
Phe Glu Val Ala Ala Arg Pro Leu Thr Ser Met Asp Val Arg Ser			
395	400	405	
Ser His Asn Ala Glu Thr Glu Val Gln Ala Ile Pro Ala Ala Thr			
410	415	420	
Asp Ile Ser Pro Glu Val Lys Glu Gly Lys Asn Ser Glu Asn Ala			
425	430	435	
Ile Thr Lys Asp Asn Asp Asp Ile Ile Leu Ser Ser Gln Leu Gln			
440	445	450	
Pro Thr Ala Thr Gly Ser Arg Ser Ser Arg Leu Ser Phe Ser Arg			
455	460	465	
His Gly His Gly Ser Gln Thr Ser Leu Gly Ser Ile Lys Arg Lys			
470	475	480	
Ser Ile Met Glu Arg Met Gly Arg Pro Thr Ser Pro Phe Met Gly			
485	490	495	
Ser Ser Phe Ser Asn Met Gly Ser Arg Ser Thr Ser Pro Thr Lys			
500	505	510	
Glu Gly Phe Ala Ser Asn Gln His Ala Thr Gly Ala Ser Val Gln			
515	520	525	
Ser Asp Glu Leu Glu Asp Ile Asp Pro Arg Ala Asn Val Val Leu			
530	535	540	
Asn Val Gly Pro Asn Met Leu Ser Val Gly Glu Ala Pro Val Glu			
545	550	555	
Ser Thr Ser Lys Glu Glu Asp Lys Asp Val Pro Asp Pro Ile Ala			

	560	565	570
Asn Ala Met Ala Glu Leu Ser Ser Ser			
575	580	585	
Met Arg Arg Arg Gln Ser			
Thr Ser Val Asp Asp Glu Ala Pro Val Ser Leu Ser Lys Thr Ser			
590	595	600	
Ser Ser Thr Arg Leu Asn Gly Leu Gly Tyr His Ser Arg Asn Thr			
605	610	615	
Ser Ile Ala Ser Asp Ile Asp Gly Val Pro Lys Lys Ser Thr Leu			
620	625	630	
Gly Ala Pro Pro Ala Ala His Thr Ser Ala Gln Met Gln Arg Met			
635	640	645	
Ser Asn Ser Phe Ala Ser Gln Thr Lys Gln Val Phe Gly Glu Gln			
650	655	660	
Arg Thr Glu Asn Ser Ala Arg Glu Ser Leu Arg His Ser Arg Ser			
665	670	675	
Asn Met Ser Arg Ser Pro Ser Pro Met Leu Ser Arg Arg Ser Ser			
680	685	690	
Thr Leu Arg Pro Ser Phe Glu Arg Ser Ala Ser Ser Leu Ser Val			
695	700	705	
Arg Gln Ser Asp Val Val Ser Pro Ala Pro Ser Thr Arg Ala Arg			
710	715	720	
Gly Gln Ser Val Ser Gly Gln Gln Arg Pro Ser Ser Ser Met Ser			
725	730	735	
Leu Tyr Gly Glu Tyr Asn Lys Ser Gln Pro Gln Leu Ser Met Gln			
740	745	750	
Arg Ser Val Ser Pro Asn Pro Leu Gly Pro Asn Arg Arg Ser Ser			
755	760	765	
Ser Val Leu Gln Ser Gln Lys Ser Thr Ser Ser Asn Thr Ser Asn			
770	775	780	
Arg Asn Asn Gly Gly Tyr Ser Gly Ser Arg Pro Ser Ser Glu Met			
785	790	795	
Gly His Arg Tyr Gly Ser Met Ser Gly Arg Ser Met Arg Gln Val			
800	805	810	
Ser Gln Arg Ser Thr Ser Arg Ala Arg Ser Pro Glu Pro Thr Asn			
815	820	825	
Arg Asn Ser Val Gln Ser Lys Asn Val Asp Pro Arg Ala Thr Phe			
830	835	840	
Thr Ala Glu Gly Glu Pro Ile Leu Gly Tyr Val Ile Ala Leu Tyr			

	845	850	855
Asp Tyr Gln Ala Gln Ile Pro Glu Glu Ile Ser Phe Gln Lys Gly			
860	865	870	
Asp Thr Leu Met Val Leu Arg Thr Gln Glu Asp Gly Trp Trp Asp			
875	880	885	
Gly Glu Ile Ile Asn Val Pro Asn Ser Lys Arg Gly Leu Phe Pro			
890	895	900	
Ser Asn Phe Val Gln Thr Val			
905			

<210> 27
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Any amino acid

<400> 27
Pro Xaa Xaa Pro
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<210> 28
<211> 1613
<212> DNA
<213> Homo sapien

<400> 28
acgatcacta tagggcgaat tgggcctcta gatgcattgt cgagcgcccg 50
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ctataggcgt cgagcgcccg cccgggcagg tctagaattc agcggcccg 150
gaattctctt tttcctcccc tcagaagctc ctctctggct cgtggctgcc 200
ttctgagtgt tgcagacggc gccggccggg aaggggggcc tgggcccagcc 250
ctgccaggac tgggacgctg ctgctgacgc ctggccctcc atcaggccag 300
cctgtggcag gagagtgagc tttgcccggc cagacgcctg aggtatgtgc 350
cccagctgca gttcaaagat gccttttgtt gcaggactt cacagcccac 400
acgggctacg aggtgctgct gcagcggctt ctggatggca ggaagatgtg 450
caaagacatg gaggagctac tgaggcagag ggcccaggcg gaggagcggt 500
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atcaactccc tgagggcctc ctttgactcc ttgaagcagc aaatggagaa 600
tgtgggcagc tcacacatcc agctggccct gaccctgcgt gaggagctgc 650

ggagtctcgaa gagttcgt gagaggcaga aggagcagag gaagaaggc 700
atggctgtcc cgagacagag tgactgcatttga gaaatgttgttccccatcatg 750
ggagttatggat gccgtcatgg accgggtcca gaagagcaag ctgtcgctct 800
acaagaaggc catggagtcc aagaagacat acgagcagaa gtgccgggac 850
gcggacgacg cgaggcaggc cttcgagcgc attagcgcca acggccacca 900
gaagcagggtg gagaagagtc agaacaaggc caggcagtgc aaggactcg 950
ccaccgaggc agagcgggta tacaggcaga gcattgcgc gctggagaag 1000
gtccgggctg agtgggagca ggagcacccgg accacctgtg aggcctttca 1050
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acagtaacca gctctccatg cagtgtgtca aggatgtga gctctacgag 1150
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tgctgcacgg aagtcccaag accacttcgt cagttctgc tggctccaca 1300
gagaccctga ccccccccccc cgagcggaat gagggtgtct acacagccat 1350
cgcagtgcag gagatacagg gaaacccggc ctcaccagcc caggactacc 1400
gggcgctcta cgattataca gcgcagaacc cagatgagct ggacctgtcc 1450
gcgggagaca tccttggagg ggaggatggc tggactg tggagaggaa 1500
cgggcagcgt ggcttcgtcc ctgggttccta cctggagaag ctggaggga 1550
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ccccagcact gtc 1613

<210> 29
<211> 400
<212> PRT
<213> Homo sapien

<400> 29
Met Met Pro Gln Leu Gln Phe Lys Asp Ala Phe Trp Cys Arg Asp
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20 25 30
Asp Gly Arg Lys Met Cys Lys Asp Met Glu Glu Leu Leu Arg Gln
35 40 45
Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile

50	55	60
Ala Arg Lys Ala Gly Gly Gln Thr Glu Ile Asn Ser Leu Arg Ala		
65	70	75
Ser Phe Asp Ser Leu Lys Gln Gln Met Glu Asn Val Gly Ser Ser		
80	85	90
His Ile Gln Leu Ala Leu Thr Leu Arg Glu Glu Leu Arg Ser Leu		
95	100	105
Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Gly Met		
110	115	120
Ala Val Pro Arg Gln Ser Asp Cys Met Glu Val Lys Ser Pro Ser		
125	130	135
Trp Glu Tyr Glu Ala Val Met Asp Arg Val Gln Lys Ser Lys Leu		
140	145	150
Ser Leu Tyr Lys Lys Ala Met Glu Ser Lys Lys Thr Tyr Glu Gln		
155	160	165
Lys Cys Arg Asp Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Ile		
170	175	180
Ser Ala Asn Gly His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys		
185	190	195
Ala Arg Gln Cys Lys Asp Ser Ala Thr Glu Ala Glu Arg Val Tyr		
200	205	210
Arg Gln Ser Ile Ala Gln Leu Glu Lys Val Arg Ala Glu Trp Glu		
215	220	225
Gln Glu His Arg Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe		
230	235	240
Asp Arg Leu Thr Ile Leu Arg Asn Ala Leu Trp Val His Ser Asn		
245	250	255
Gln Leu Ser Met Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu		
260	265	270
Val Arg Leu Thr Leu Glu Gly Cys Ser Ile Asp Ala Asp Ile Asp		
275	280	285
Ser Phe Ile Gln Ala Lys Ser Thr Gly Thr Glu Pro Pro Arg Phe		
290	295	300
Ser Gly Leu Leu His Gly Ser Pro Lys Thr Thr Ser Ser Ala Ser		
305	310	315
Ala Gly Ser Thr Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu		
320	325	330
Gly Val Tyr Thr Ala Ile Ala Val Gln Glu Ile Gln Gly Asn Pro		

	335	340	345
Ala Ser Pro Ala Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala			
350	355		360
Gln Asn Pro Asp Glu Leu Asp Leu Ser Ala Gly Asp Ile Leu Glu			
365	370		375
Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly			
380	385		390
Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu			
395	400		

<210> 30
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<400> 73
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